

GGGGGATCATGGAAGCTGATAAAGATGACACACAACAAATTCTTAAGGAGCATTGCGCCAGATGAA  
TTTATAAAAGATGAACAAAATAAGGGACTAATTGATGAAATTACAAAGAAAAATATTCAACTAAA  
GAAGGAGATCCAAAAGCTTGAAACGGAGTTACAAGAGGCTACCAAAGAATTCCAGATTAAAGAGG  
ATATTCCTGAAACAAAGATGAAATTCTTATCAGTTGAAACTCCTGAGAATGACAGCCAGTTGTCA  
AATATCTCCTGTTTCGTTTCAAGTGAGCTCGAAAGTTCCTTATGAGATACAAAAGGACAAGCACT  
TATCACCTTTGAAAAAGAAGAAGTTGCTCAAAATGTGGTAAGCATGAGTAAACATCATGTACAGA  
TAAAAGATGTAAATCTGGAGGTTACGGCCAAGCCAGTTCCATTAAATTCAGGAGTCAGATTCCAG  
GTTTATGTAGAAGTTTCTAAAATGAAAATCAATGTTACTGAAATTCCTGACACATTGCGTGAAGA  
TCAAATGAGAGACAACTAGAGCTGAGCTTTTCAAAGTCCCGAAATGGGAGGCGGAGANGTGGAC  
CGCGTGGGACTATGACAGACAGTCCGGGAGTGCAATCATCACGTTTGGNGGAGATTGGGAGTGGC  
TGACANN (SEQ ID NO: 4)

**Figure 1**

Hou c6/#1

CGGAGTTACAAGAGGCTACCAAAGAATTCCAGATTAAAGAGGATATTCCTGAAACAAAGATGAAA  
TTCTTATCAGTTGAAACTCCTGANAATGACAGCCAGTTGTCAAATATCTCCTGTTTCGTTTCAAGG  
TGAGCTCGAAAGTTCCTTATGAGATACAAAAAGGACAATGCACTTATCACCTTTGAAAAAGGAAG  
AAGTTGCTCAAAATGTGNGTAANGCATGAGTAAACATCATGTACAGATAATAAGATGTAAATCTG  
GAGGTTACGGCCAAAGCCAAGTTCCATTAATATTCAAGGAGTCANGATTCCAGNGTTTATGCTAG  
AANGTTTCTAAAAATGANAATCAATGGTTACTGGAAATTCCTGGACACATTGCGNTGAAAGATCA  
AGATGACGAAGACAACTAAGAAGCTGAGCTTTTCAAAAGTCCCGAAANATGGAAGAGCGGTAGA  
GGGTGGNACCGCGTGNGANCTATGACAAGACAAGNCCGGGGGAAGNTGCAGTCCATCACGTTTGTN  
NGAAGATTGGANGTNGGCTGACCAANGAATTTTGAAAAAGGAGANGAATTACCCCTCTTTANGAG  
TAANATCAAAACCCTGCCATAANAAGTTNACTGGTTTCNCCCATTACACAGNAN  
TTACANNTTGANCAANANTANNCAGGATAATTTNCAGGGGAANAATCTNAAGNATGGCAAGNTGA  
CTTCTGGACAANGGT (SEQ ID NO: 5)

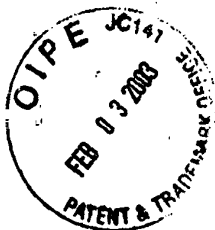
**Figure 2**

Hou c17/#2

c6/#1	1	HEGRGI	DKDDTQQILKEHSPDEFIKDEQNKGL	ITKKNIQLKKEIQKLETELQEA
Hou/Nmi	1	-----	DKDDTQQILKEHSPDEFIKDEQNKGL	ITKKNIQLKKEIQKLETELQEA
c6/#1	61	TKEFQIKEDIPETKMKFLSVETPENDS	QLSNISCSFQVSSKVPYEQKGQALITFEKEEV	
Hou/Nmi	55	TKEFQIKEDIPETKMKFLSVETPENDS	QLSNISCSFQVSSKVPYEQKGQALITFEKEEV	
c6/#1	121	AQNVVSMKHHVQIKDVNLEVTA	KPVPLNSGVRFQVYVEVSKMKINVTEIPDTLREDQMR	
Hou/Nmi	115	AQNVVSMKHHVQIKDVNLEVTA	KPVPLNSGVRFQVYVEVSKMKINVTEIPDTLREDQMR	
c6/#1	181	DKLELSFSKSRNGRRRCGPR	GTMTDSPGVQSSRLVEIGS	-----
Hou/Nmi	175	DKLELSFSKSRNGGGEV.DR	VVDYDRQSGSAVITFVEIGV	DKILKKKEYPLYINQTCHRV
c6/#1	221	-----	-----	-----
Hou/Nmi	234	TVSPYTEIHLKKYQIFSGTSKRTVLLTGMEGIQMDEEIVEDLINIH	FQRAKNGGGEVDVV	
c6/#1	221	-----	(SEQ 10 NO:6)	
Hou/Nmi	294	KCSLGQPHIAYFEE	(SEQ 10 NO:7)	

Figure 3





AGCAGGTGCTGCAACAAAAGGAGCACACGATCAACATGGAGGAGTGCCGGCTGCGGGTGCAGGTC  
CAGCCCTTGGAGCTGCCCATGGTCACCACCATCCAGGTGTCCAGCCAGTTGAGTGGCCGGAGGGT  
GTTGGTCACTGGATTTCCCTGCCAGCCTCAGGCTGAGTGAGGAGGAGCTGCTGGACAANCTANAGA  
TCTTCTTTGGCAAGACTAGGAACGGAGGTGGCNATGTGGACNTTCGGGANCTACTGCCAGGGANT  
GTCATGCTGGGGTTTGCTAGGGATGGAGTGGCTCANCCTGTGTGCCAAATCGGCCATTTACAGT  
GCCACTGGGTGGGCAGCANGTCCCTCTGAGAGTCTCTCCGTATGTGAATGGGGANATCCAGANGG  
CTGANATCAGGTCNCAGCCANTTCCCCGCTCGGTACTGGTGCTCAACATTCCTGATATCTTGGAT  
GGCCCGGAGCTGCATGACGTCCTGGANATCCACTTCCAGAANCCACCCGCGGGGGCGGAGATGT  
AAGACGCCCTGACAGTCGTACCCCAAGGACAACAGGGCCTAACAGTCTTCACCTCCTGAATCAAG  
GCTANGGGCCTCCCCCTTCTCATCTCCCCACCCCCCGCCAAAGGTTCTCAANACTGGGCCTG  
GGCTTTNTG (SEQ ID NO. 8)

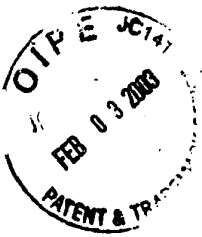
**Figure 4**

IFP35 c14/#1

CCAAAGTGGCTGAGCAGGTGCTGCAACAAAAGGAGCACACGATCAACATGGAGGAGTGCCGGCTGCGGGTGC  
AGGTCCAGCCCTTGGAGCTGCCCATGGTCACCACCATCCAGGTGTCCAGCCAGTTGAGTGGCCGGAGGGTGT  
TGGTCACTGGATTTCTGCCAGCCTCAGGCTGAGTGAGGAGGAGCTGCTGGACAAGCTAGAGATCTTCTTTG  
GCAAGACTAGGAACGGAGGTGGCGATGTGGACGTTCTGGGAGCTACTGCCAGGGAGTGTGATGCTGGGGTTTG  
CTAGGGATGGAGTGGCTCAGCGTCTGTGCCAAATCGGCCAAGTTCACAGTGCCACTGGGTGGGCANCAAGTC  
CCTCTGAGAGTCTCTCCGTATGTGAATGGGGAGATCCAGAAGGCTGAGATCAGGTCGCANCCAGTTCCCCNC  
TCGGTACTGGGTGCTCAACATTCCTGATATCTTGGATTGGCCCGGAGCTGCATNACGTCCTGGANATCAACT  
TCANAAGCCCACCCGCCGGGGCNGNGAGGTANAAGGCCTGACATCNTTACCCCAAAGGACAGCATGGNCCTA  
ACAGTCCTCACCTCCNAATCANGCTNNGGGGCTNCCCTTCTANCNTCCCCAACTG (SEQ ID NO: 9)

**Figure 5**

IFP35 c33/#2



GGATCCACTGCCCTCTGCTTGCGGGCTCTGCTCTGATCACCTTTGATGACCCCAAAGTGGCTGAG  
CAGGTGCTGCAACAAAAGGAGCACACGATCAACATGGAGGAGTGCCGGCTGCGGGTGCAGGTCCA  
GCCCTTGGAGCTGCCCATGGTCACCACCATCCAGGTGATGGTGTCCAGCCANTTGAGTGGCCGGA  
GGGTGTTGGTCACTGGATTTCTGCCAGCCTCAGGCTGANTGAGGAGGAGCTGCTGGACAAGCTA  
TGAGATCTTCTTTGGCAANACTANGAACGGANGTGGCGATGTGGACGTTCTGGGAGCTACTGCCAG  
GGAGTGTCATGCTGGGGTTTGCTACGGATGGAGTGGCTCAGCGTCTGTGCCAAATCGGCCAGTTC  
ACAAGTGCCACTGGGTGGGCAGCAAGTCCCTCTGAGAGTCTCTCCGTATGTGANTGGNGAGATCA  
GAATGCTGANATTAAGTCGCATCCAATTCCTCGCTCNGGTACTGGTGCTCANNATCCTGANATCT  
TGGATTGGCCCCNGANTNCATGANATCTGGNAGATTCAATTNCANAAGTCCANCCNNCNGNGNCG  
GGAAGTANANGCCCGANANTTCNTNNCNTANGGNCAGCANNGCCTG (Seq 10 NO: 10)

**Figure 6**

IFP35 c51/#3

331fn	1	-----
In35_Human	1	MSAPLDAALHALQEEQARLKMLWDLQQLRKELGDSFKDKVPFVSPKIPLVFRGHTQQDP
C51	1	-----
331fn	1	-----HCGPKVAEQVLQOKEHTINMEECLRLRVQVQPLELPM
In35_Human	61	EVPKSLVSNLRIHCPLLAGSALITFDDPKVAEQVLQOKEHTINMEECLRLRVQVQPLELPM
C51	1	-----HEGRIHCPLLAGSALITFDDPKVAEQVLQOKEHTINMEECLRLRVQVQPLELPM
331fn	37	VTTIQ..VSSQLSGRRVLVTGFPA SLRLSEEELLDKLEIFFGKTRNGGGDVDVRELLPGS
In35_Human	121	VTTIQ..VSSQLSGRRVLVTGFPA SLRLSEEELLDKLEIFFGKTRNGGGDVDVRELLPGS
C51	54	VTTIQVMVSSXLSGRRVLVTGFPA SLRLXEEELLDKL*DLLWQXXERXWRC.....
331fn	95	VMLGFARDGVAQRLCQIGQVHSATGWASSPSESLSVCEWGDPE-----
In35_Human	179	VMLGFARDGVAQRLCQIGQFTVPLGGQQVPLRVSPYVNGEIQKAEIRSQPVPRSVLVLNI
C51	104	.....GRSGATARECHAGVCYGWSGSASVPMRPFVHKCHWVGSKSL*ESLRM*XRSEC*X
331fn	139	----- (SEQ ID NO: 11)
In35_Human	239	PDILDGPELHDVLEIHFOKPTRGGGGRCPDSRTPTAGPSSLHL----- (SEQ ID NO: 12)
C51	156	*VASNSSLXYWCSXS*XLGLAPXXMXSGRFNXXSPXXXXGKXXPXXSXXXXXSXA (SEQ ID NO: 13)

Figure 7



Abp2	1	RLRNGHVGISFVPKETGEHLVHVKKNGQHVASSPIPVVISQSEIGDASRVVRVSGQGLHEG
C50	1	-----
C57	1	-----
Abp2	61	HTFEPAEFIIDTRDAGYGGLSLSIEGFSKVDINTEDLEDGTCRVTYC <b>PTTEPGNYIINIKE</b>
C50	1	-----
C57	1	-----HEGR <b>PTTEPGNYIINIKE</b>
Abp2	121	<b>ADQHVPGPSFVSVKVTGEGRVKESITRRRRAPSVANVGSHCDLSLKIPETISIQDNTAQVTS</b>
C50	1	-----
C57	18	<b>ADQHVPGPSFVSVKVTGEGRVKESITRRRRAPSVANVGSHCDLSLKIPETISIQDNTAQVTS</b>
Abp2	181	<b>PSGKTHEAEIVEGENHTYTCIRFVPAEMGTHTVSVKYKGQHVPGSPFQFTVGPLGEGGAHX</b>
C50	1	-----
C57	78	<b>PSGKTHEAEIVEGENHTYTCIRFVPAEMGTHTVSVKYKGQHVPGSPFQFTVGPLGEGGAHX</b>
Abp2	241	<b>VRAGGPGLEKAEAGVPAEFS.IWTREAGAGGLATAVEQPKAEISFEDRKDGSCGVAYVV</b>
C50	1	-----
C57	138	<b>VRAGGPGLEKES*SWASRIQYLGPGLVLEKWPILSXAPLXISLLRTARTAPVVLMEV</b>
Abp2	300	<b>QEPGDYEVSVKFNEEHIPDSPFVVPVASPSGDARRLTVSSLQESGLKVNQPASFAVSLNG</b>
C50	1	-----
C57	197	<b>KEPSD*XNPXQVSTKEHX-----</b>
Abp2	360	<b>AKGAIDAKVHSPSGALEECYVTEIDQDKYAVRFIPRENGVYLIDVKFNGTHIPGSPFKIR</b>
C50	1	-----
C57	214	-----
Abp2	420	<b>VGEFGHGGDPGLVSAYGAGLEG.GVTGNPAEFVVNTSNAGAGALSVTIDGPSKVKMDCQE</b>
C50	1	-----HEGRGV <b>TGNPAEFVVNTSNAGAGALSVTIDGPSKVKMDCQE</b>
C57	214	-----
Abp2	479	<b>CPEGYRVITYTPMAPGSYLISIKYGGPYHIGGSPFKAKVTGPRLVSNHSLHETSSVFVDSL</b>
C50	42	<b>CPEGYRVITYTPMAPGSYLISIKYGGPYHIGGSPFKAKVTGPRLVSNHSLHETSSVFVDSL</b>
C57	214	-----
Abp2	539	<b>TKATCAPQHGA PGPGPADASKVVAKGLGLSKAYVGOKSSFTVDCSKAGNNMLLVGVHGP</b>
C50	102	<b>TKATCAPHGA PGPGPADASKVVAKGLGLSKAYVCHKSSFTVDCSKACIIMLLVGVHGPW</b>
C57	214	-----
Abp2	599	<b>TPCEILVKHVGS.RLYSVSYLLKDKGE.YTLVVKWGHEHIGSPYRVVVP-(SEQ ID NO: 14)</b>
C50	162	<b>TPCEILVKARGQPALQRLTCFKDKGEVHTGGQNGGDYQIPCKPLPFCGCP-(SEQ ID NO: 15)</b>
C57	214	----- <b>(SEQ ID NO: 16)</b>

Figure 8

